



Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: 2568)

```
1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTTCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTGA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCATAA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC
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Figure 2A. The cDNA (SEQ ID. NO. :2569) and amino acid sequence (SEQ ID. NO. :2570) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

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1 gccggcctccagcagcgggcgcgcgggcgcgagcacgacccccactctcctgcgggccgcg
61 ggtggagcagcgcgagcccgctcgctgagccggccggggcggggagatgagttgcggc
121 cccgcggcagcgcggccaggatggggagggacgcgcggcactgccctcgagaactggcgct
181 ccggtgaagtaggcgcgcggccgctccgcctcccccaagccggttcgcacccgcggccgcg
1 M A G S G A W K R L K S M L R K
241 tcagcctctgcccATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCCGCTGTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCGGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGAAAGGCCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAATCACCAACCAAAAGATTACCTTTGGATTT
177 H R L E V L S A M I S V L L V Y I L M G
781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA
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197 F L L Y E A V Q R T I H M N Y E I N G D
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGAT
217 I M L I T A A V G V A V N V I M G F L L
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG
237 N Q S G H R H S H S H S L P S N S P T R
961 AACCAGTCTGGTCACCGTCACTCCCATTTCCCACTCCCTGCCTTCAAATTTCCCTACCAGA
257 G S G C E R N H G Q D S L A V R A A F V
1021 GGTTCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTA
277 H A L G D L V Q S V G V L I A A Y I I R
1081 CATGCTTTGGGAGATTTGGTACAGAGTGTTGGTGTGCTAATAGCTGCATACATCATACGA
297 F K P E Y K I A D P I C T Y V F S L L V
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
317 A F T T F R I I W D T V V I I L E G V P
1201 GCTTTTACAACATTTTGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA
337 S H L N V D Y I K E A L M K I E D V Y S
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA
357 V E D L N I W S L T S G K S T A I V H I
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTACATA
377 Q L I P G S S S K W E E V Q S K A N H L
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA
397 L L N T F G M Y R C T I Q L Q S Y R Q E
1441 TTATTGAACACATTTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAA
417 V D R T C A N C Q S S S P *
1501 GTGGACAGAACTTGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttgggaa
1561 ctcctgccttatttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatga
1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc
1681 cagcctgacagtgctagtctctgttttaattggtaaaaggagactttgccataattttcaga
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag
1801 aagacaatccaagatcatacttcattaacttgacagagtacgtgtcttaaggaagcatc
1861 aagaattcaatattttgcatttaaaaatactttttaaggccattttatattaagccagtgc
1921 tggaaaactgaattttttttattatgtataataatctcgacacccagcttctggaattgc
1981 tgctttctttttacagaaaattactaccaacagattttcaggaagtactagtagttatccc
2041 aaaagtggaataagcatgtattcctaagtgtttcagaaatgttttatttcacacataagt
2101 cttaatgttattgttatgattatactttataaacaaccttttccagatgctacagggttt
2161 tgaatctcaaagttaacattttttcattatgttaactcttagaaccaaacttttattttatt
2221 gtggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag
2281 ttagtcttaaaactcaaattactatatgatgatttaaaacaaaataaaagagcgaggatgg
2341 ggaaaaaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :2571) and amino acid sequence (SEQ ID. NO. :2572) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGAAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATTCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTGGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
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1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtctctgttttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :2573) and amino acid sequence (SEQ ID. NO. :2574) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATTCCCCTACCAGAGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATAACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT
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Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND ENCODED ZINC TRANSPORTER
PROTEIN ENTITLED 108P5H8 USEFUL IN TREATMENT
AND DETECTION OF CANCER

REPLACEMENT SHEET 6/38

341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattgttttagcattgctgaatt
1321 cactttatttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc
1441 ctgacagtgctagtcctctgtttaatggtaaaaggagactttgccataattttcagatgaa
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

Figure 3:

Figure 3A. Amino acid sequence corresponding to 108P5H8 v.1 (SEQ ID NO: 2570) and 108P5H8 v.2 (SEQ ID. NO. :2572). The 108P5H8 v.1 and 108P5H8 v.2 proteins have 429 amino acids.

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1  MAGSGAWKRL  KSMLRKDDAP  LFLNDTSAFD  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILTLTLL  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAFTT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGM YRCTIQL  QSYRQEV DRT
421  C A N C Q S S S P *

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Figure 3B. Amino acid sequence corresponding to 108P5H8 v.3 (SEQ ID. NO. :2574). The 108P5H8 v.3 protein has 429 amino acids.

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1  MAGSGAWKRL  KSMLRKDDAP  LFLNDTSAFE  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILTLTLL  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAFTT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGM YRCTIQL  QSYRQEV DRT
421  C A N C Q S S S P *

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Figure 4:

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8. (SEQ ID NOs: 2569, 2571 & 2573). Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15	16	30	31	45	46	60	61	75	76	90
v.1	GCCGGCCTCCAGCAG	CGGGCGGGCGGGCG	CGAGCACGACCCAC	TCTCTGGGGCGCG	GGTGAGCAGCGCGA	CCCCGCCTCGCTGAG					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
91	105	106	120	121	135	136	150	151	165	166	180
v.1	CCGGCCGGGGCGGG	GAGATGAGTTGCGC	CCCGCGCAGCGGCC	CAGGATGGGAGGGA	CGCGCGGCACTGCC	TCGAGAACTGGCGCT					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
181	195	196	210	211	225	226	240	241	255	256	270
v.1	CCGGTGAAGTAGGCG	CCGCCGGCGGTCGCG	CTCCCCCAAGCCGTT	CCGCACCGCGGCGCG	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
271	285	286	300	301	315	316	330	331	345	346	360
v.1	TGGAAGCGCCTCAAA	TCTATGCTAAGGAAG	GATGATGCGCCGCTG	TTTTTAAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGGCGGGG					
v.2	TGGAAGCGCCTCAAA	TCTATGCTAAGGAAG	GATGATGCGCCGCTG	TTTTTAAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGGCGGGG					
v.3	TGGAAGCGCCTCAAA	TCTATGCTAAGGAAG	GATGATGCGCCGCTG	TTTTTAAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGGCGGGG					
361	375	376	390	391	405	406	420	421	435	436	450
v.1	GACGAGGGGCTTTCT	CGGTTCAACAACAACTT	CGAGTTGTGTGGCC	GATGACGGTTCGGAA	GCCCCGGAAAGGCCT	GTTAACGGGGCGGCAC					
v.2	GACGAGGGGCTTTCT	CGGTTCAACAACAACTT	CGAGTTGTGTGGCC	GATGACGGTTCGGAA	GCCCCGGAAAGGCCT	GTTAACGGGGCGGCAC					
v.3	GACGAGGGGCTTTCT	CGGTTCAACAACAACTT	CGAGTTGTGTGGCC	GATGACGGTTCGGAA	GCCCCGGAAAGGCCT	GTTAACGGGGCGGCAC					
451	465	466	480	481	495	496	510	511	525	526	540
v.1	CCGACCCCTCCAGGCC	GACGATGATTCCCTTA	CTGGACCAAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
v.2	CCGACCCCTCCAGGCC	GACGATGATTCCCTTA	CTGGACCAAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
v.3	CCGACCCCTCCAGGCC	GACGATGATTCCCTTA	CTGGACCAAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					

541	555	556	570	571	585	586	600	601	615	616	630
v.1	AACTGCAGCAAACAG	AGAGAGATACTGAAG	CAGAGAAAGGTGAAA	CCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTTCATGATT					
v.2	AACTGCAGCAAACAG	AGAGAGATACTGAAG	CAGAGAAAGGTGAAA	CCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTTCATGATT					
v.3	AACTGCAGCAAACAG	AGAGAGATACTGAAG	CAGAGAAAGGTGAAA	CCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTTCATGATT					
631	645	646	660	661	675	676	690	691	705	706	720
v.1	GGAGAACTTGTAGGT	GGATACATTGCAAAAT	AGCCTAGCAATCATG	ACAGATGCACCTTCAT	ATGTTAACTGACCTA	AGGCCATCATACTC					
v.2	GGAGAACTTGTAGGT	GGATACATTGCAAAAT	AGCCTAGCAATCATG	ACAGATGCACCTTCAT	ATGTTAACTGACCTA	AGGCCATCATACTC					
v.3	GGAGAACTTGTAGGT	GGATACATTGCAAAAT	AGCCTAGCAATCATG	ACAGATGCACCTTCAT	ATGTTAACTGACCTA	AGGCCATCATACTC					
721	735	736	750	751	765	766	780	781	795	796	810
v.1	ACCCTGCTTGCTTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATTT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
v.2	ACCCTGCTTGCTTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATTT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
v.3	ACCCTGCTTGCTTTG	TGGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATTT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT					
811	825	826	840	841	855	856	870	871	885	886	900
v.1	AGTGTGCTGTTGGTG	TATATACTTATGGGA	TTCTCTTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACCTAT	GAAATAAATGGAGAT					
v.2	AGTGTGCTGTTGGTG	TATATACTTATGGGA	TTCTCTTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACCTAT	GAAATAAATGGAGAT					
v.3	AGTGTGCTGTTGGTG	TATATACTTATGGGA	TTCTCTTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACCTAT	GAAATAAATGGAGAT					
901	915	916	930	931	945	946	960	961	975	976	990
v.1	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCAAGTCTGGTCAC	CGTCACTCCCATTCC					
v.2	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCAAGTCTGGTCAC	CGTCACTCCCATTCC					
v.3	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCAAGTCTGGTCAC	CGTCACTCCCATTCC					
991	1005	1006	1020	1021	1035	1036	1050	1051	1065	1066	1080
v.1	CACCTCCCTGCCCTTCA	AATCCCTACCAGA	GTTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTTGTA					
v.2	CACCTCCCTGCCCTTCA	AATCCCTACCAGA	GTTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTTGTA					
v.3	CACCTCCCTGCCCTTCA	AATCCCTACCAGA	GTTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTTGTA					
1081	1095	1096	1110	1111	1125	1126	1140	1141	1155	1156	1170
v.1	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGAATAC	AAGATTGCTGACCCC					
v.2	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGAATAC	AAGATTGCTGACCCC					
v.3	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGAATAC	AAGATTGCTGACCCC					
1171	1185	1186	1200	1201	1215	1216	1230	1231	1245	1246	1260

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND ENCODED ZINC TRANSPORTER
PROTEIN ENTITLED 108P5H8 USEFUL IN TREATMENT
AND DETECTION OF CANCER

REPLACEMENT SHEET 10/38

v.1	ATCTGTACATACGTA	TTTTCATTACTTGTG	GCCTTTACAACATTT	CGAATCATATGGGAT	ACAGTACTTATAATA	CTAGAAGGTTGTGCCA					
v.2	ATCTGTACATACGTA	TTTTCATTACTTGTG	GCCTTTACAACATTT	CGAATCATATGGGAT	ACAGTACTTATAATA	CTAGAAGGTTGTGCCA					
v.3	ATCTGTACATACGTA	TTTTCATTACTTGTG	GCCTTTACAACATTT	CGAATCATATGGGAT	ACAGTACTTATAATA	CTAGAAGGTTGTGCCA					
1261	1275	1276	1290	1291	1305	1306	1320	1321	1335	1336	1350
v.1	AGCCATTTGAATGTA	GACTATATCAAAGAA	GCCTTGATGAAAATA	GAAGATGTATATTCA	GTCGAAGATTTAAAT	ATCTGGTCTCTCACT					
v.2	AGCCATTTGAATGTA	GACTATATCAAAGAA	GCCTTGATGAAAATA	GAAGATGTATATTCA	GTCGAAGATTTAAAT	ATCTGGTCTCTCACT					
v.3	AGCCATTTGAATGTA	GACTATATCAAAGAA	GCCTTGATGAAAATA	GAAGATGTATATTCA	GTCGAAGATTTAAAT	ATCTGGTCTCTCACT					
1351	1365	1366	1380	1381	1395	1396	1410	1411	1425	1426	1440
v.1	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTCATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
v.2	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTCATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
v.3	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTCATCTAAATGG	GAGGAAGTACAGTCC	AAAGCAAACCATTTA					
1441	1455	1456	1470	1471	1485	1486	1500	1501	1515	1516	1530
v.1	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTGAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAACTTGT	GCAAAATTTGCAGAGT					
v.2	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTGAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAACTTGT	GCAAAATTTGCAGAGT					
v.3	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTGAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAACTTGT	GCAAAATTTGCAGAGT					
1531	1545	1546	1560	1561	1575	1576	1590	1591	1605	1606	1620
v.1	TCTAGTCCCTAATTT	TATGTATT	TTGGG	AACTCCTG	CTTATTTATCCTGCA	GTCAACAGACTTGAGA	GCAATAAATGCAAAAC				
v.2	TCTAGTCCCTAATTT	TATGTATT	TTGGG	GACTCCTG	CTTATTTATCCTGCA	GTCAACAGACTTGAGA	GCAATAAATGCAAAAC				
v.3	TCTAGTCCCTAATTT	TATGTATT	TTGGG	CAATGCTGAATTCAC	CTTATTTATCCTGCA	GTCAACAGACTTGAGA	GCAATAAATGCAAAAC				
1621	1635	1636	1650	1651	1665	1666	1680	1681	1695	1696	1710
v.1	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCCAGCCTG	ACAGTGGTAGTCTCT					
v.2	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCCAGCCTG	ACAGTGGTAGTCTCT					
v.3	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCGTATCAAGC	ATCAGTCTCTCAAAC	AGTTGCCCCAGCCTG	ACAGTGGTAGTCTCT					
1711	1725	1726	1740	1741	1755	1756	1770	1771	1785	1786	1800
v.1	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTCAGATGAAGAT	GTITCCCCAACACTG	TTTACAGAAATGAGAT	GTGACTCTACAGAT					
v.2	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTCAGATGAAGAT	GTITCCCCAACACTG	TTTACAGAAATGAGAT	GTGACTCTACAGAT					
v.3	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTCAGATGAAGAT	GTITCCCCAACACTG	TTTACAGAAATGAGAT	GTGACTCTACAGAT					
1801	1815	1816	1830	1831	1845	1846	1860	1861	1875	1876	1890

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REPLACEMENT SHEET 11/38

v.1	ACCTCATAGAAGACA	ATCCAAGATCATACT	TCATTAACTTGACAG	AGTACGTGTCTTAAA	GGAAGCATCAAGAAT	TCAATATTTCATTT	
v.2	ACCTCATAG-----	-----	-----	-----	-----	-----	
v.3	ACCTCATAG-----	-----	-----	-----	-----	-----	
1891	1905 1906	1920 1921	1935 1936	1950 1951	1965 1966	1980	
v.1	AAAAAATACTTTTAA	GGCCATTTTATATTA	AGCCAGTGTGGAAA	ACTGAATTTTTTTTA	TTATGTATAATAATC	TCGACACCCAGCTTC	
v.2	-----	-----	-----	-----	-----	-----	
v.3	-----	-----	-----	-----	-----	-----	
1981	1995 1996	2010 2011	2025 2026	2040 2041	2055 2056	2070	
v.1	TGGAATTGCTGCTTT	CTTTTACAGAAAT	ACTACCCAACAGATT	TCAGGAAGTACTAGT	AGTTATCCCAAAAGT	GGAATAAGCATGTAT	
v.2	-----	-----	-----	-----	-----	-----	
v.3	-----	-----	-----	-----	-----	-----	
2071	2085 2086	2100 2101	2115 2116	2130 2131	2145 2146	2160	
v.1	TCCTAAGTGTTCAG	AAATGTTTATTTC	CACATAAGTCTTAAT	GTTATTGTTATGATT	ATACTTTATAAACAA	CCTTTCCAGATGCT	
v.2	-----	-----	-----	-----	-----	-----	
v.3	-----	-----	-----	-----	-----	-----	
2161	2175 2176	2190 2191	2205 2206	2220 2221	2235 2236	2250	
v.1	ACAGGGTTTGAATC	TCAAAGTTAACATTT	TTCATTATTGTGAAT	CTTAGAACCAAAATCT	TTATTATTGTGGTC	ACTGTTATTAAATGA	
v.2	-----	-----	-----	-----	-----	-----	
v.3	-----	-----	-----	-----	-----	-----	
2251	2265 2266	2280 2281	2295 2296	2310 2311	2325 2326	2340	
v.1	TTTAGGAAATACTTT	CAATATTATTCTGAA	TGGCTGAAGTTAGTC	TTAAACTCAAATTAC	TATATGATGATTTAA	AACAAAATAAAAGAG	
v.2	-----	-----	-----	-----	-----	-----	
v.3	-----	-----	-----	-----	-----	-----	
2341	2355 2356	2370					
v.1	CGAGGATGGGGAAA	AAAAAAAAAAAAAAA	AAA	2364			
v.2	-----	-----	---	1548			
v.3	-----	-----	---	1557			

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Figure 4B Amino Acid Alignment of the 3 variants of 108P5H8 (SEQ ID NOS: 2570, 2572 & 2574)

1	15	16	30	31	45	46	60	61	75	76	90
v.1	MAGSGAWKRLKSMRL	KDDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHTLOADDD	LLDQDLPLTNSQLSL					
v.2	MAGSGAWKRLKSMRL	KDDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHTLOADDD	LLDQDLPLTNSQLSL					
v.3	MAGSGAWKRLKSMRL	KDDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHTLOADDD	LLDQDLPLTNSQLSL					
91	105	106	120	121	135	136	150	151	165	166	180
v.1	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAILLTLLALWLSS	KSPTKRFTFGFHRLE					
v.2	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAILLTLLALWLSS	KSPTKRFTFGFHRLE					
v.3	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAILLTLLALWLSS	KSPTKRFTFGFHRLE					
181	195	196	210	211	225	226	240	241	255	256	270
v.1	VLSAMISVLLVYIIM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDSLA					
v.2	VLSAMISVLLVYIIM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDSLA					
v.3	VLSAMISVLLVYIIM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDSLA					
271	285	286	300	301	315	316	330	331	345	346	360
v.1	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDYIK	EALMKIEDVYSVEDL					
v.2	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDYIK	EALMKIEDVYSVEDL					
v.3	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDYIK	EALMKIEDVYSVEDL					
361	375	376	390	391	405	406	420	421			
v.1	NIWLSLTSKGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLNLTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						
v.2	NIWLSLTSKGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLNLTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						
v.3	NIWLSLTSKGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLNLTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						

Figure 5: 108P5H8 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

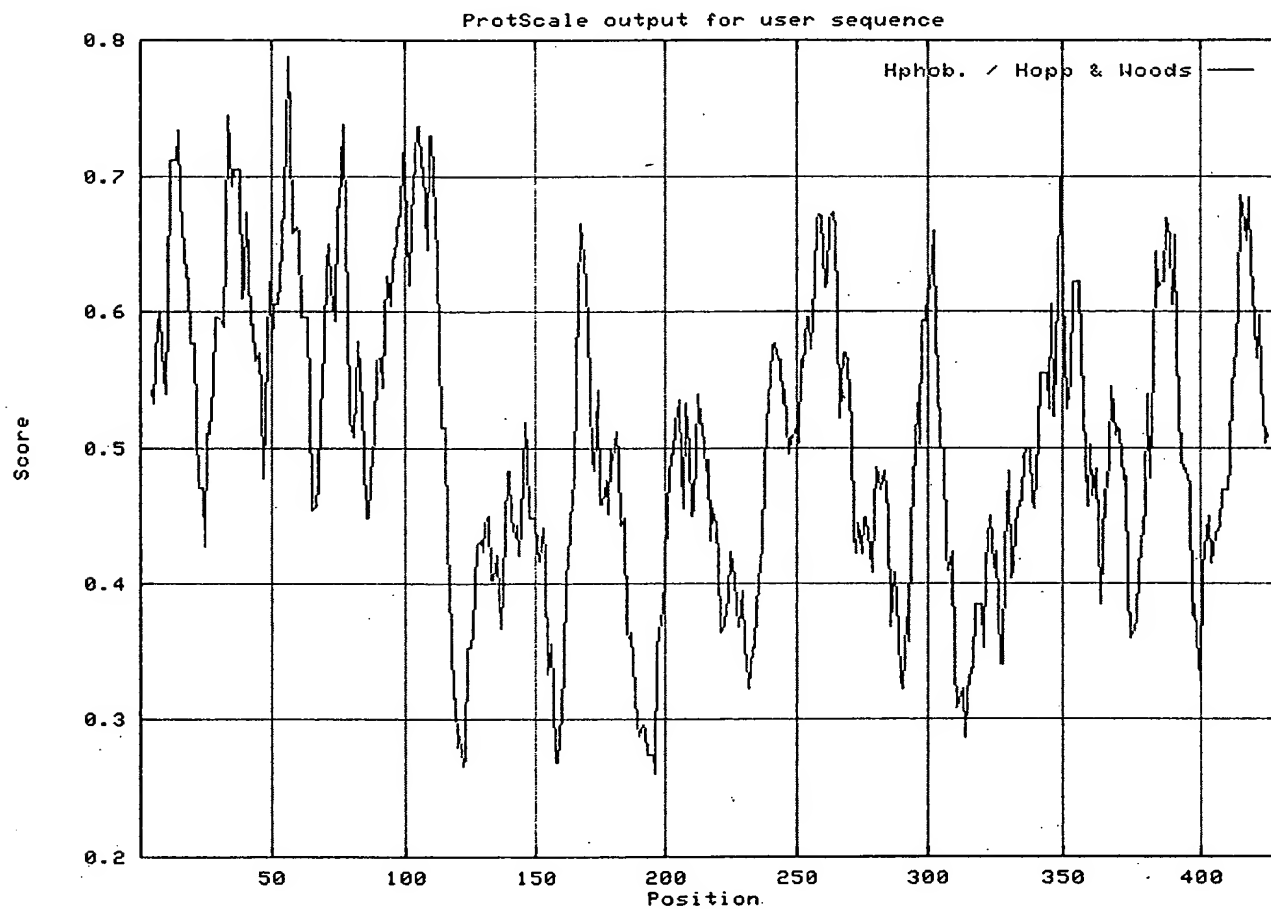


Figure 6: 108P5H8 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

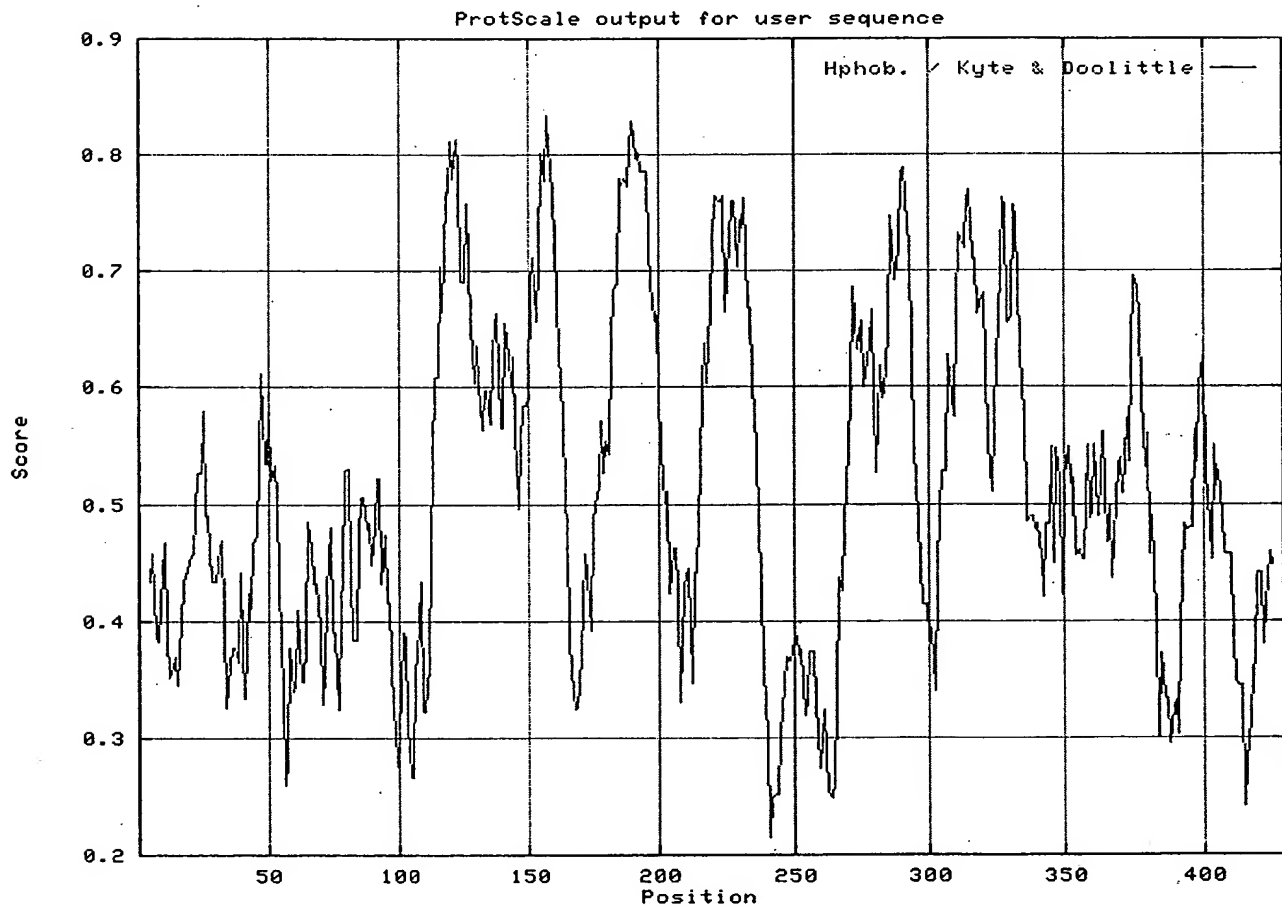


Figure 7: 108P5H8 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

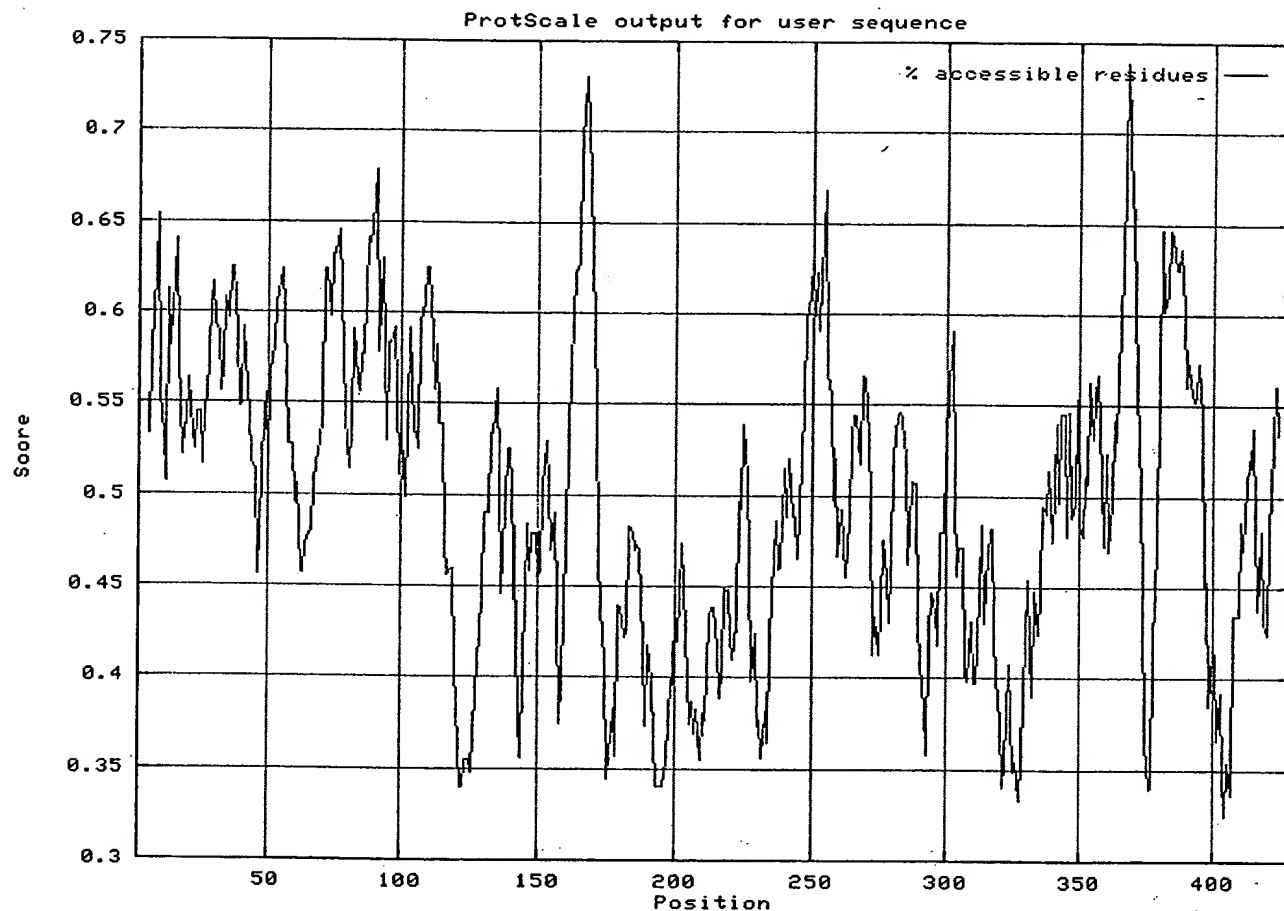


Figure 8: 108P5H8 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

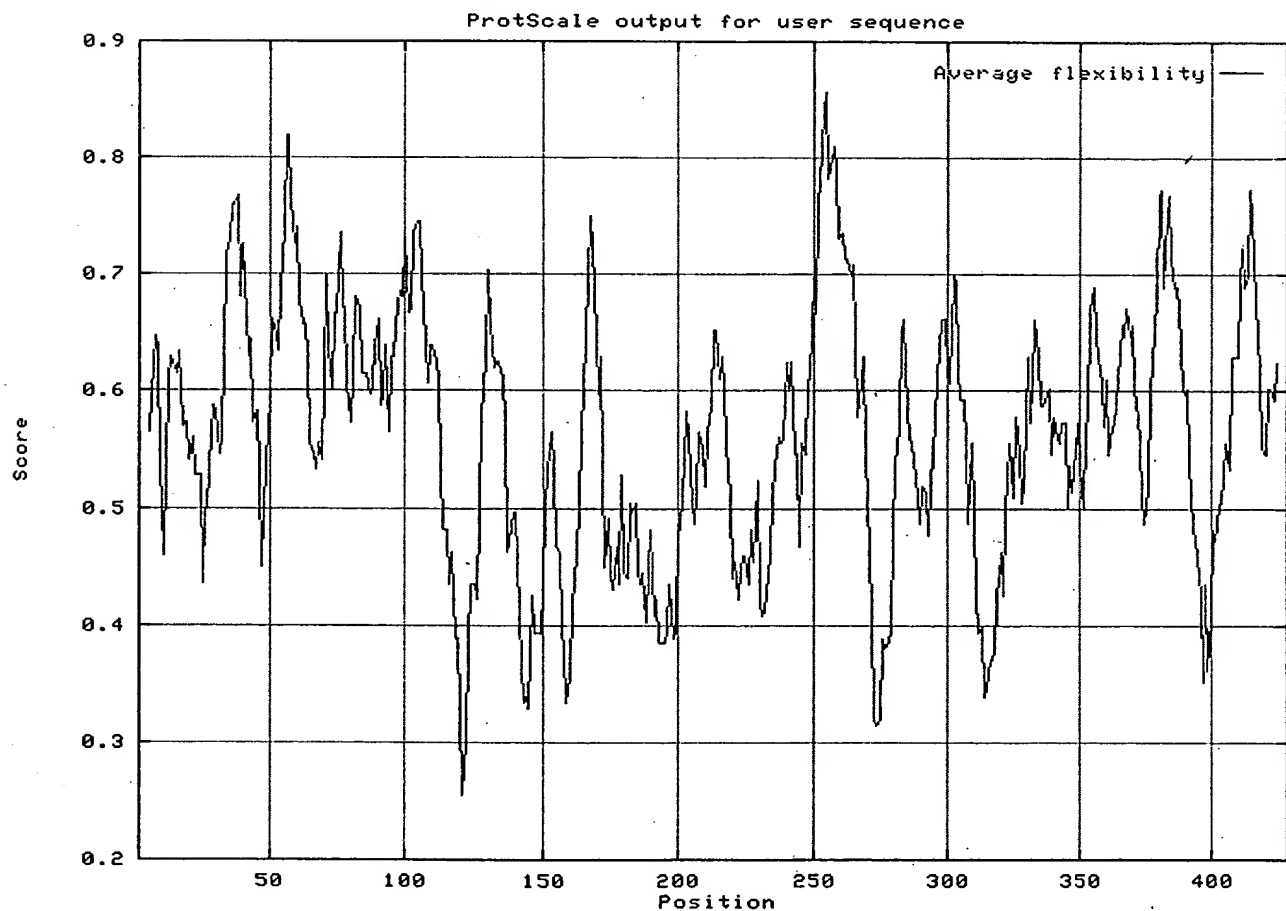


Figure 9: 108P5H8 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

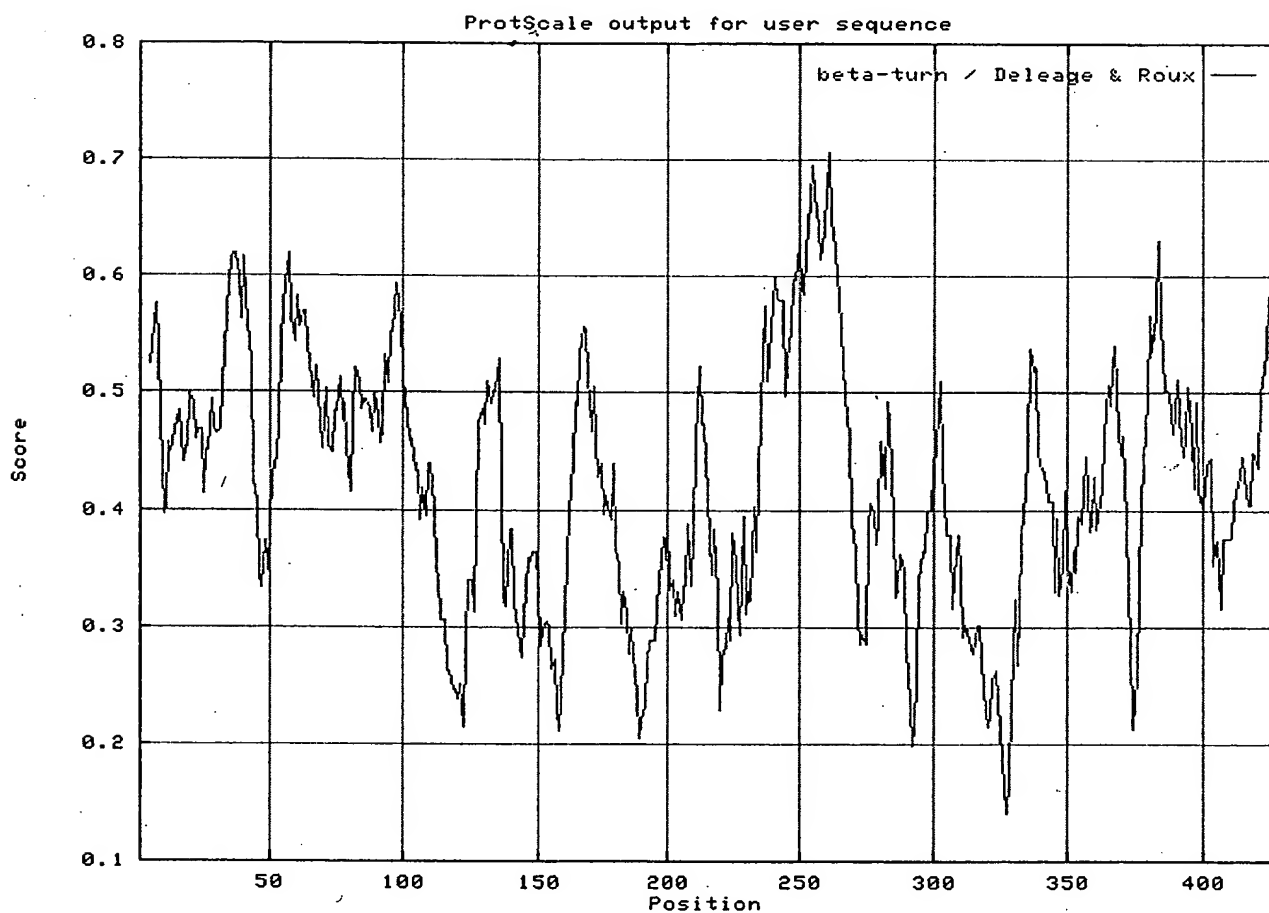


Figure 10

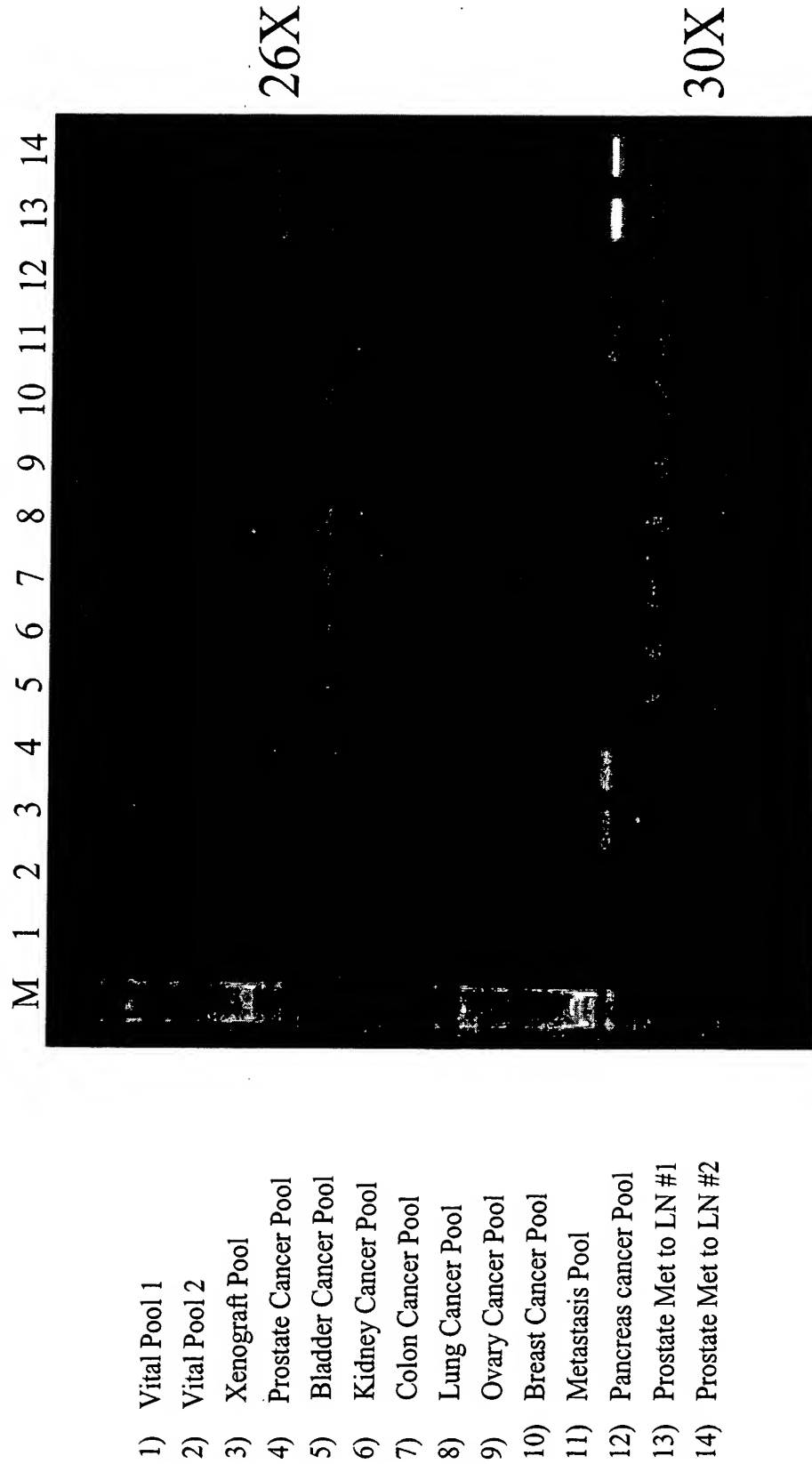


Figure 11

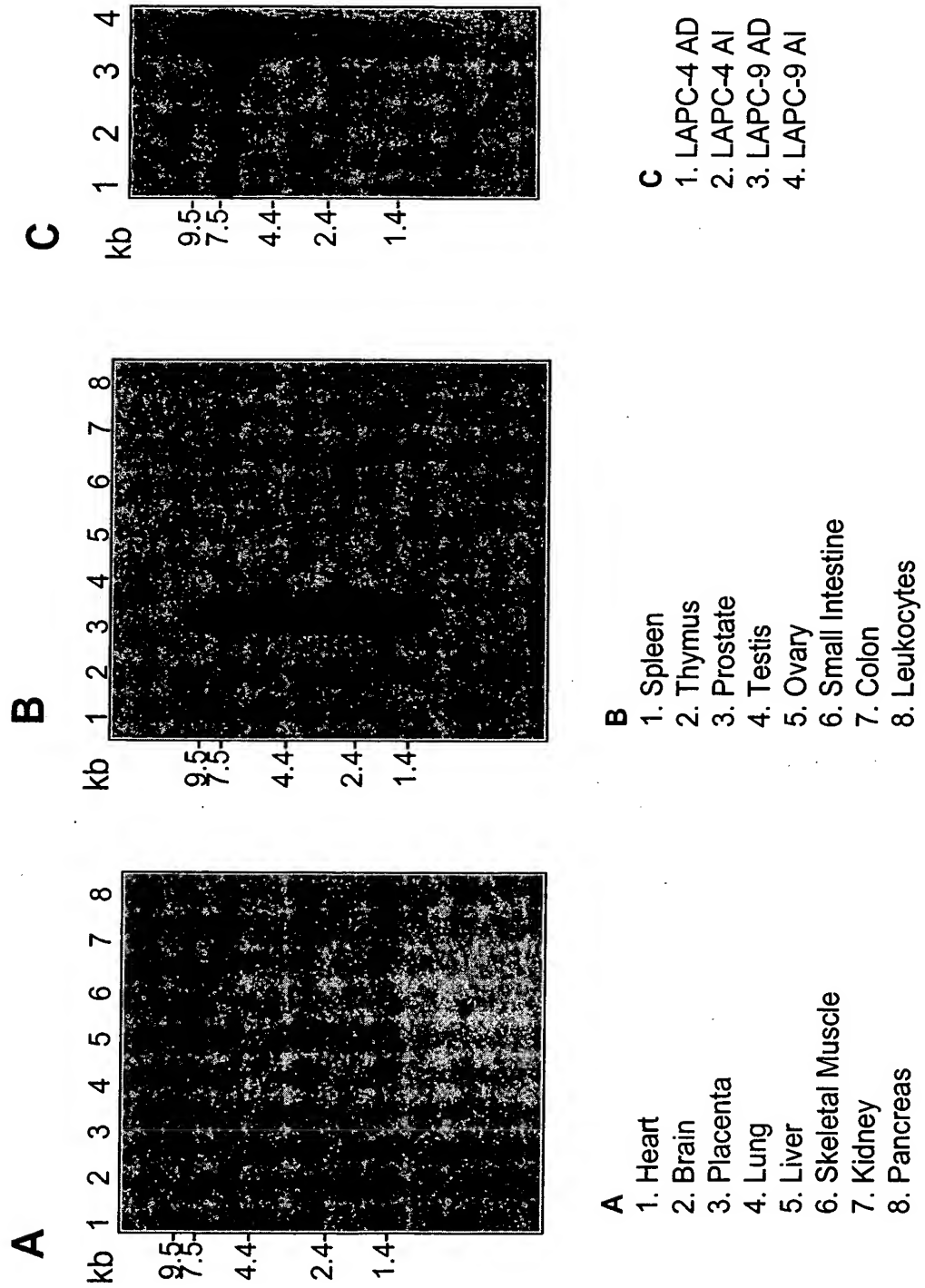


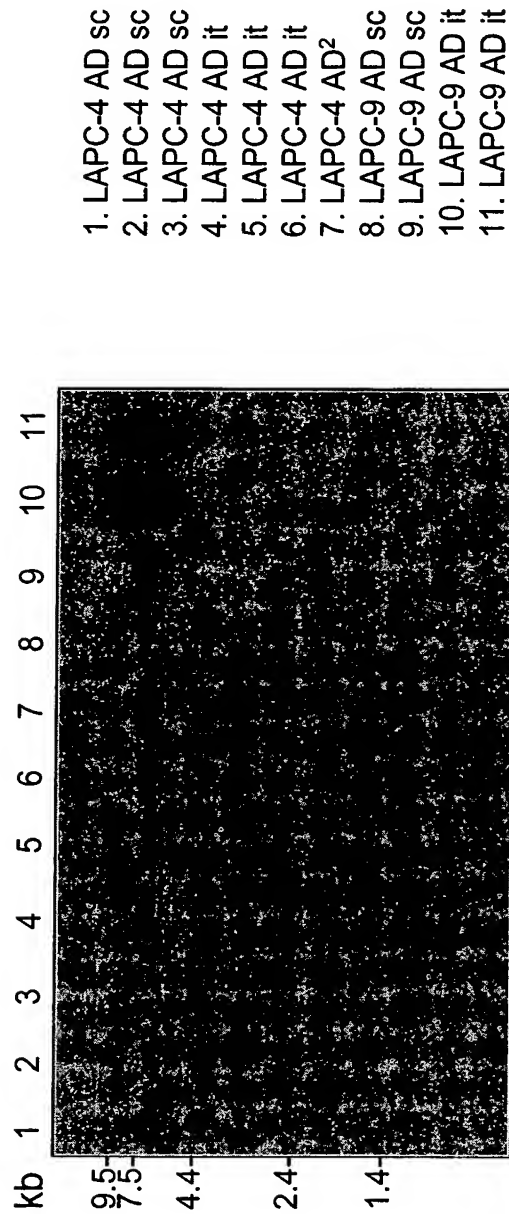
Figure 12

Figure 13

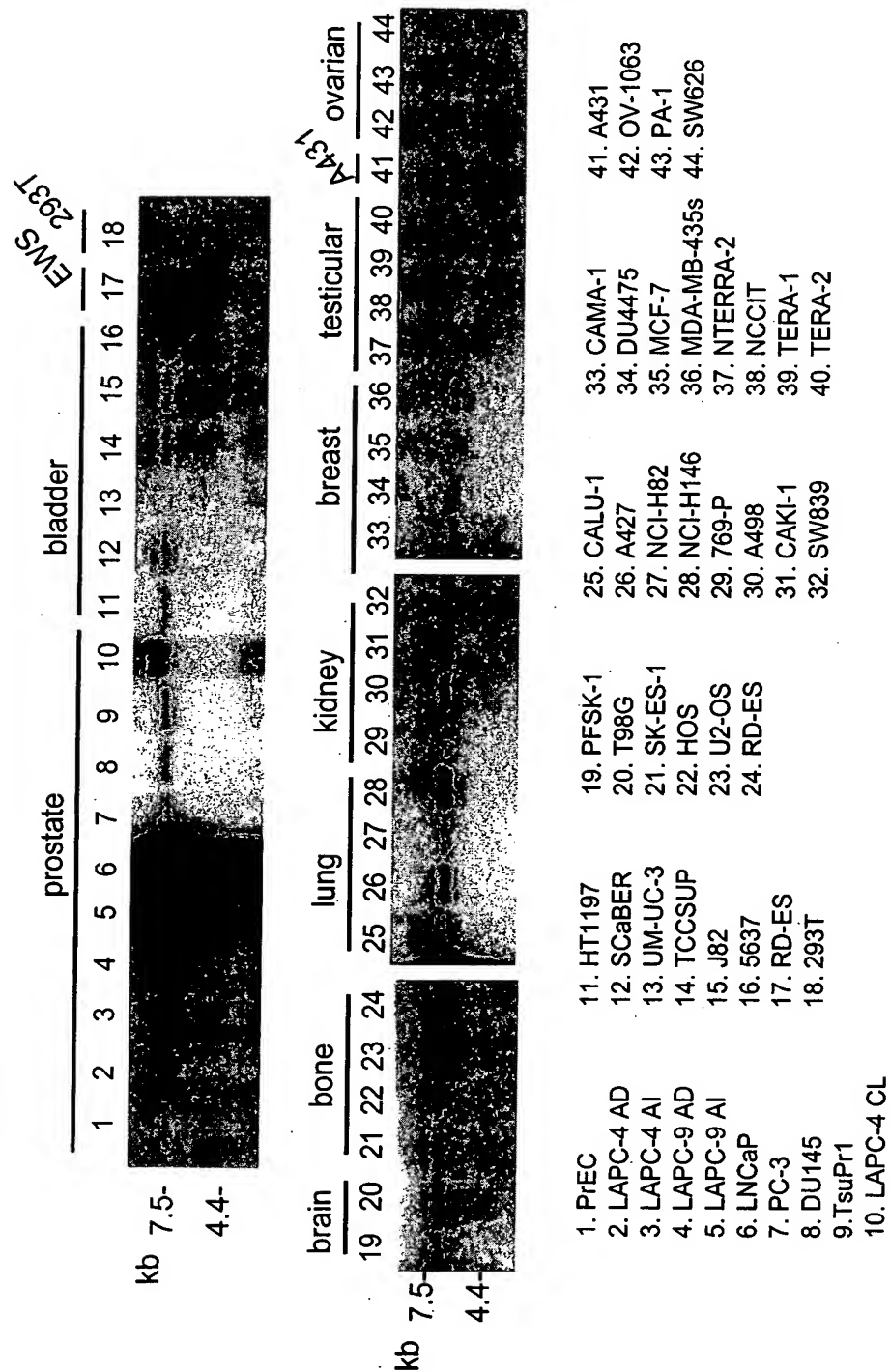


Figure 14

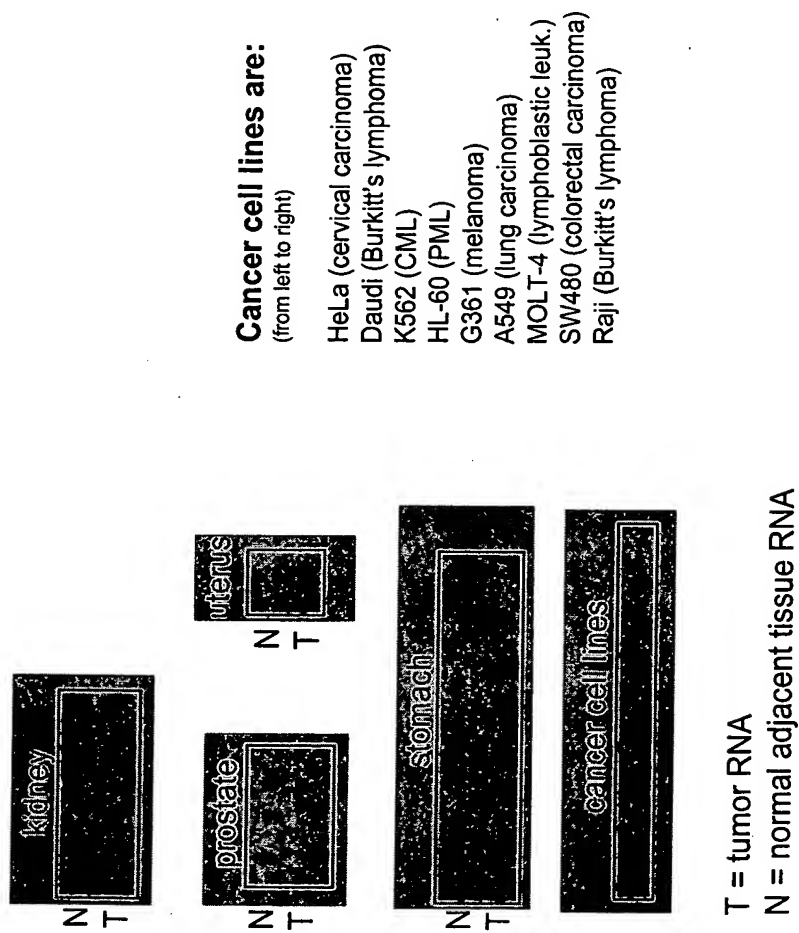


Figure 15

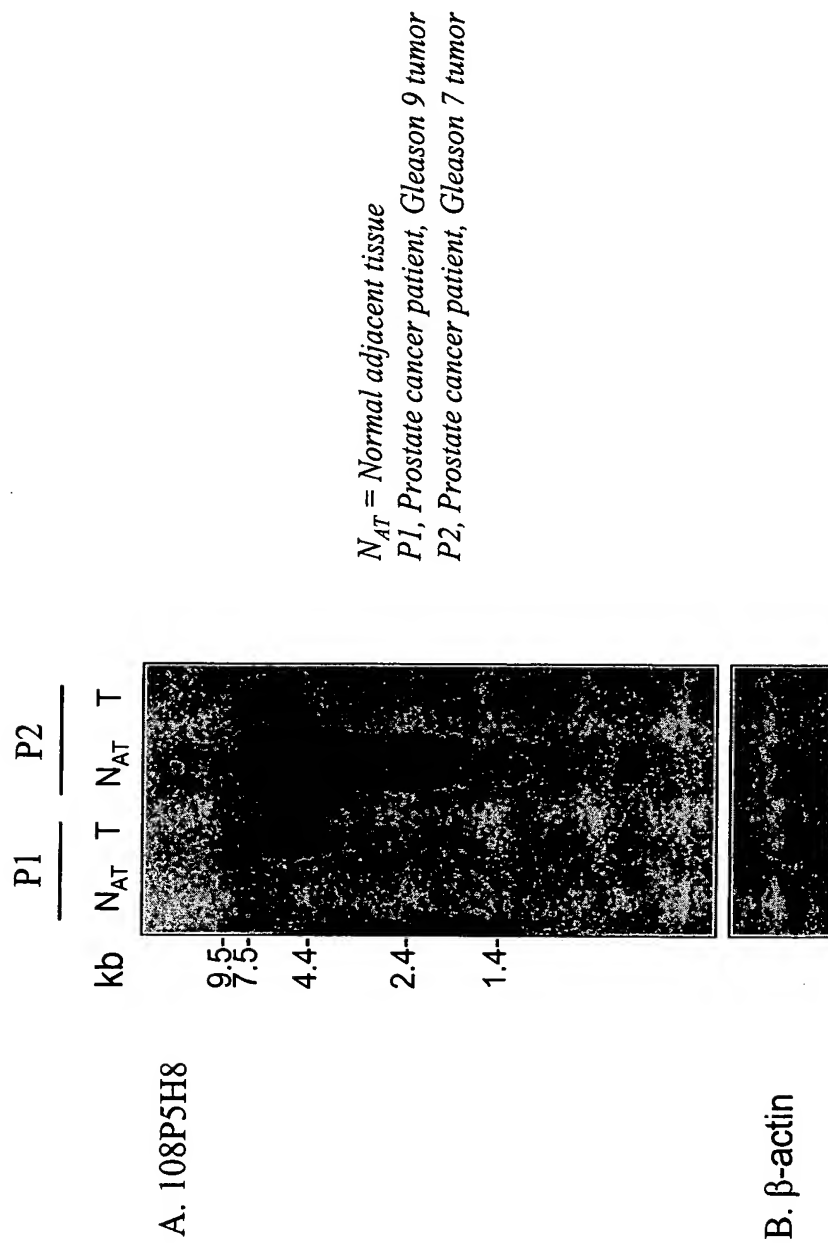


Figure 16

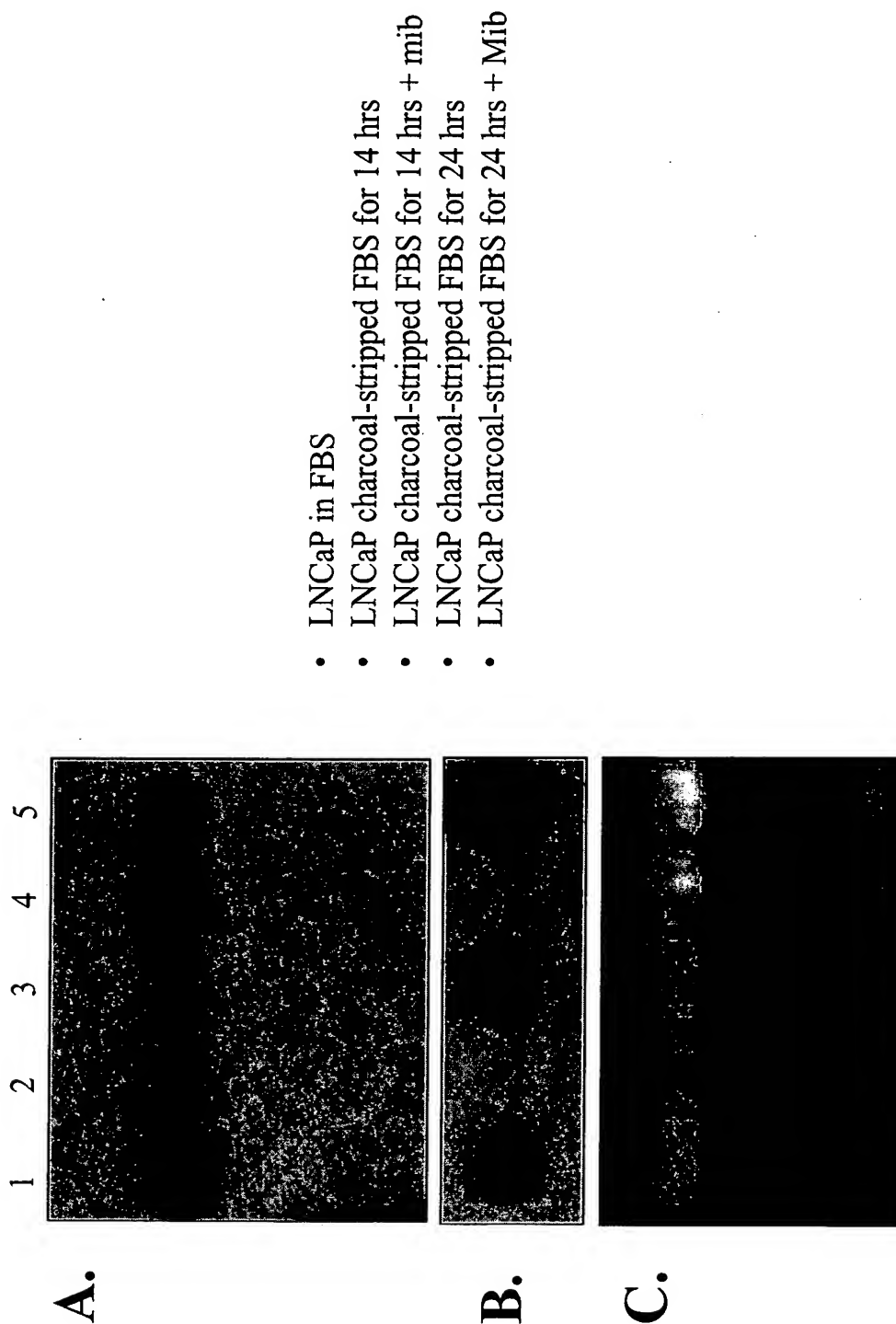
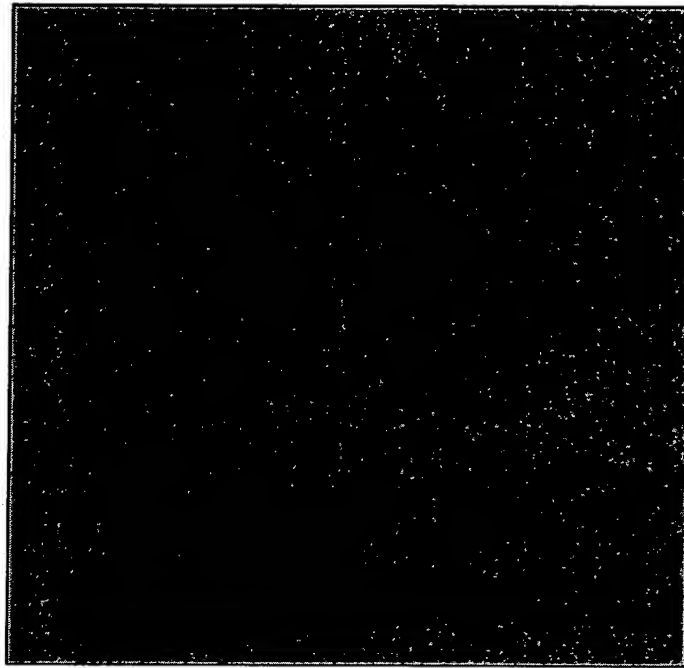


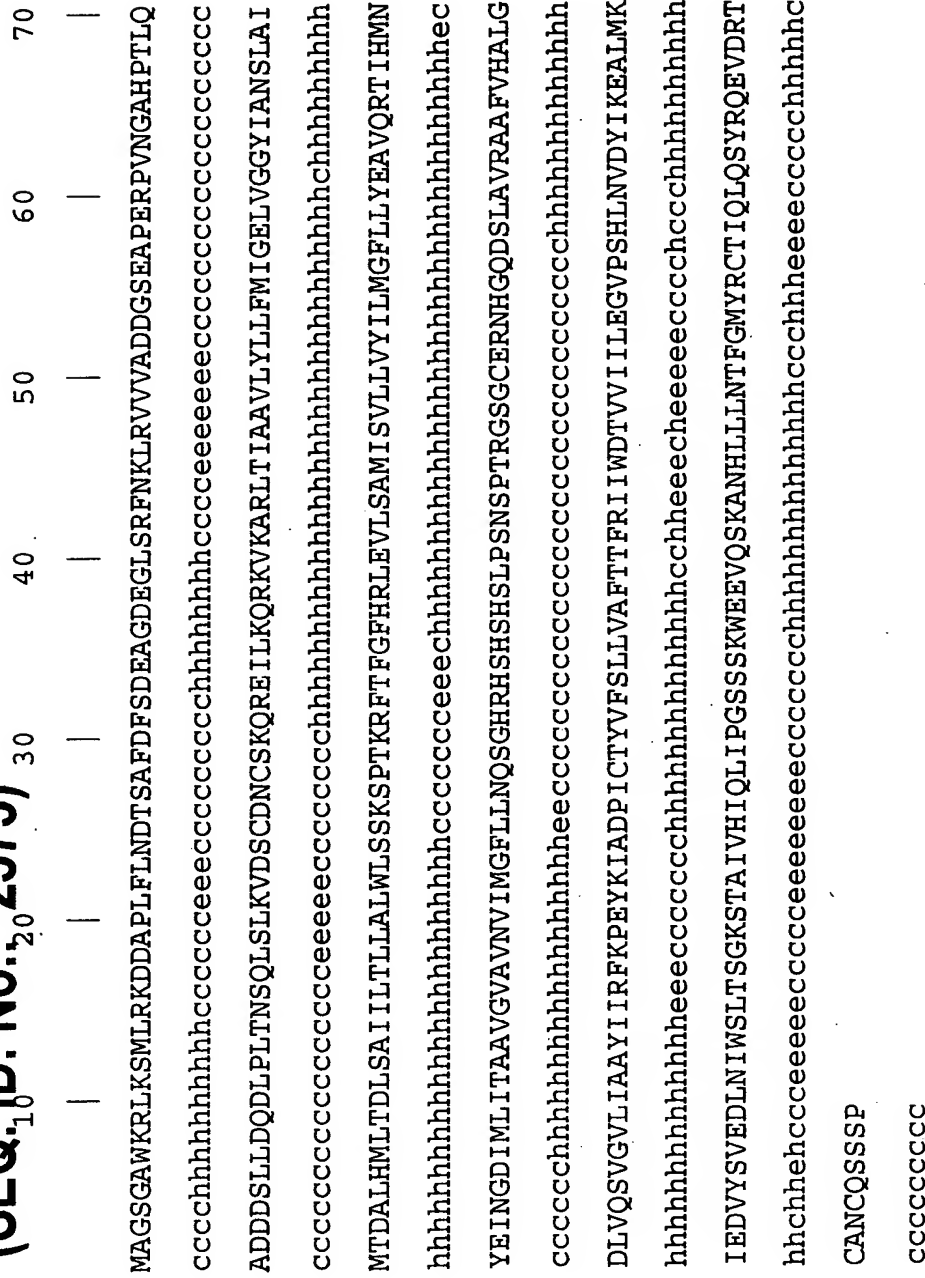
Figure 17

Met1 Met2 NB NK NL NBr NO NPa



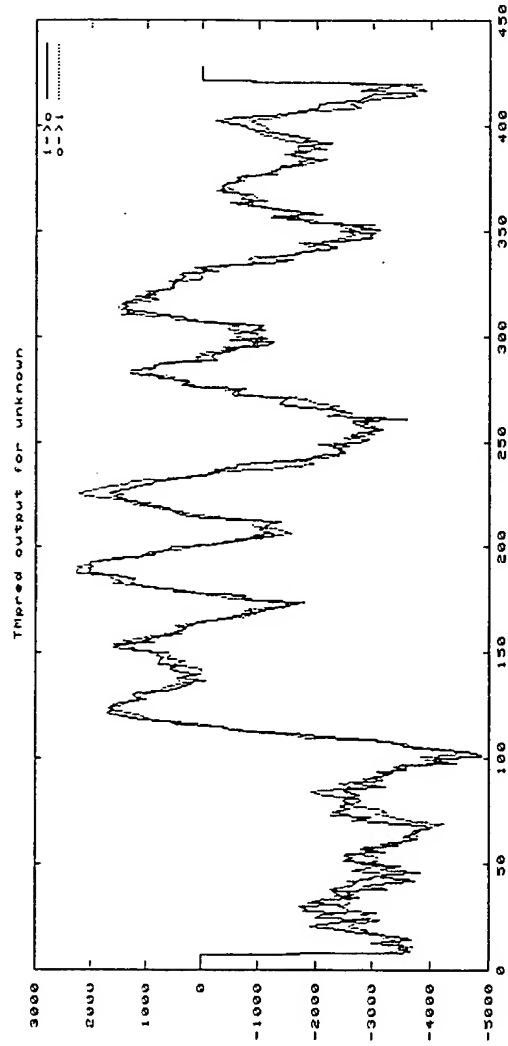
*Met1 = Prostate cancer metastasis to lymph
 node from patient 1*
*Met2 = Prostate cancer metastasis to lymph
 node from patient 2*
NB = normal bladder
NK = normal kidney
NL = normal lung
NBr = normal breast
NO = normal ovary
NPa = normal pancreas

Figure 18: Secondary structure analysis of 108P5H8 (SEQ. ID. No.: 2575)



c: random coil (38.46%)
e: extended strand (11.66%)
h: alpha helix (49.88%)

Figure 19



Transmembrane domains

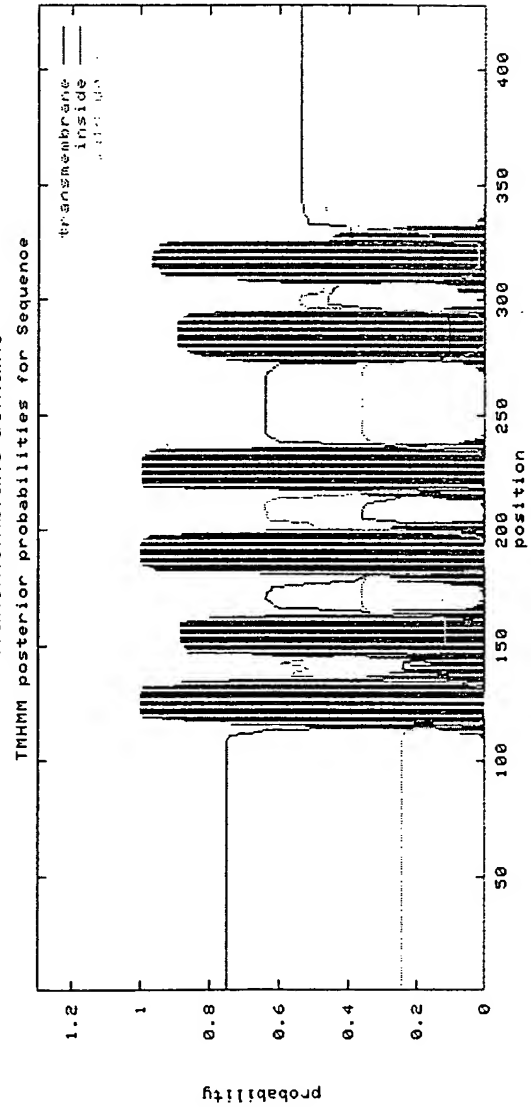


Figure 20

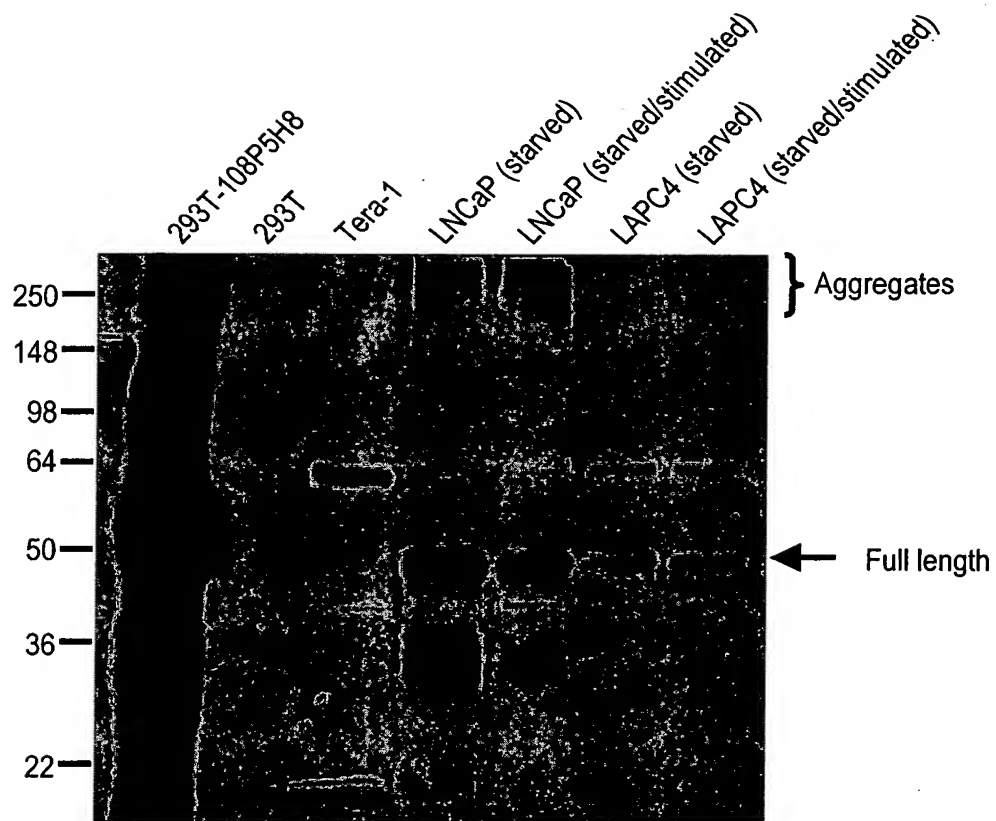


Figure 21

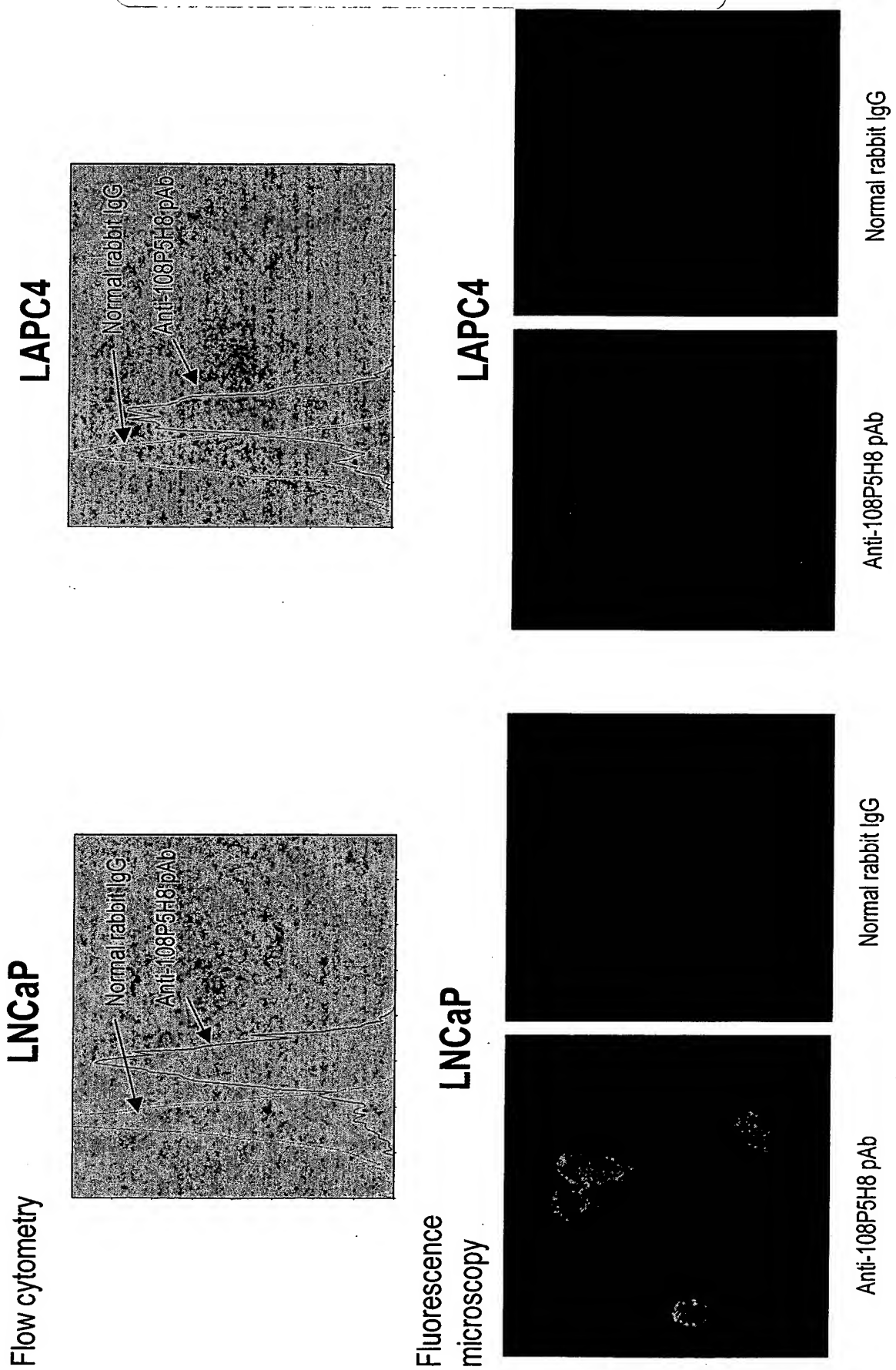
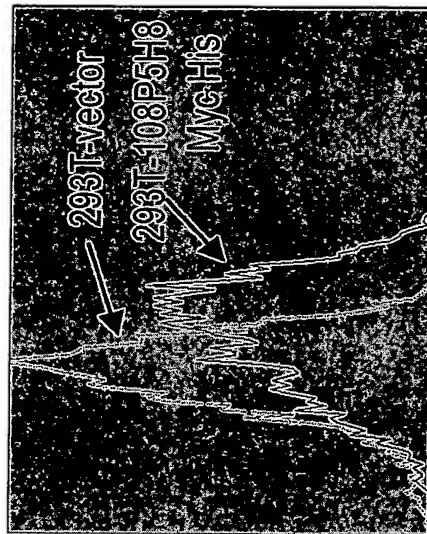


Figure 22

Flow cytometry

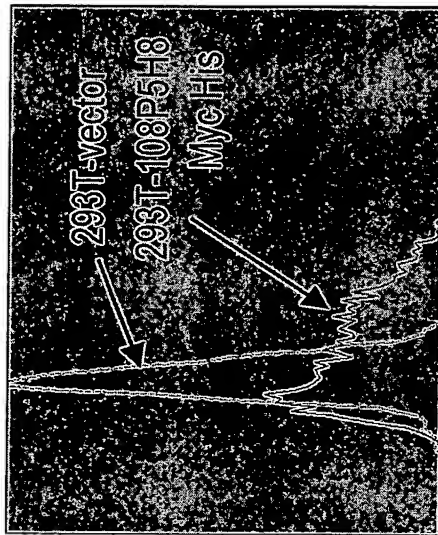


Anti-His pAb

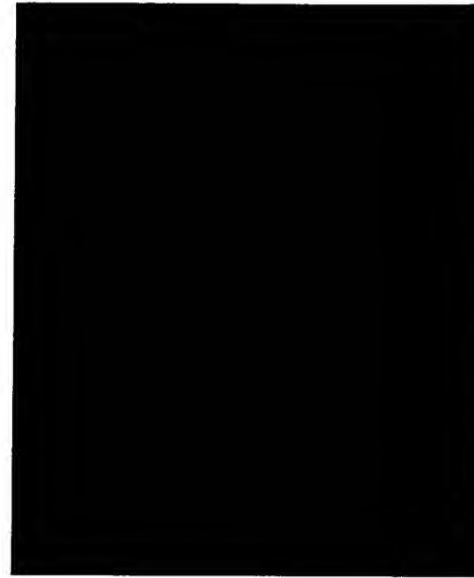
Fluorescence
microscopy



293T-108P5H8



Anti-108P5H8 pAb



293T-vector

Anti-108P5H8 pAb

Figure 23

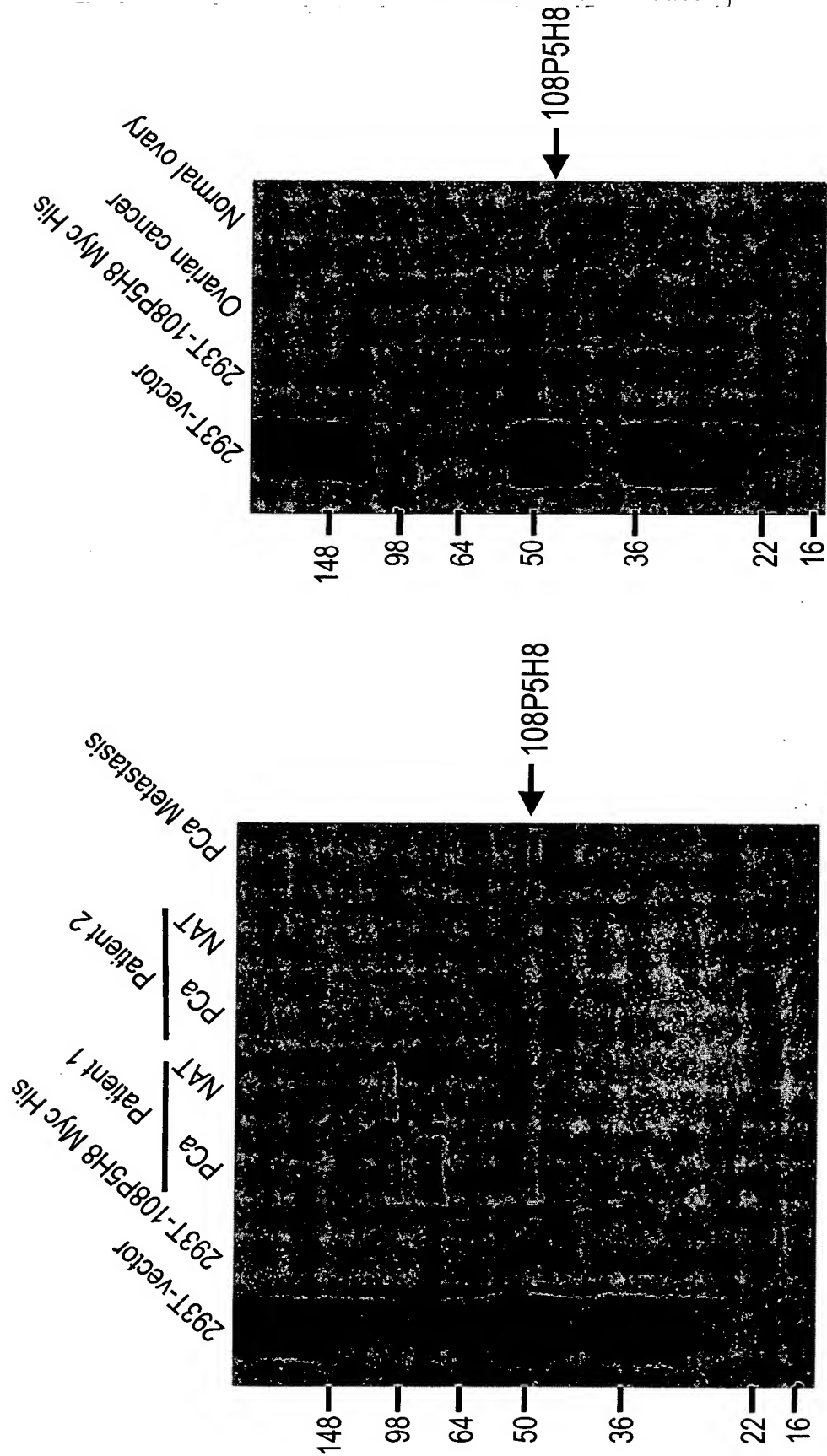


Figure 24

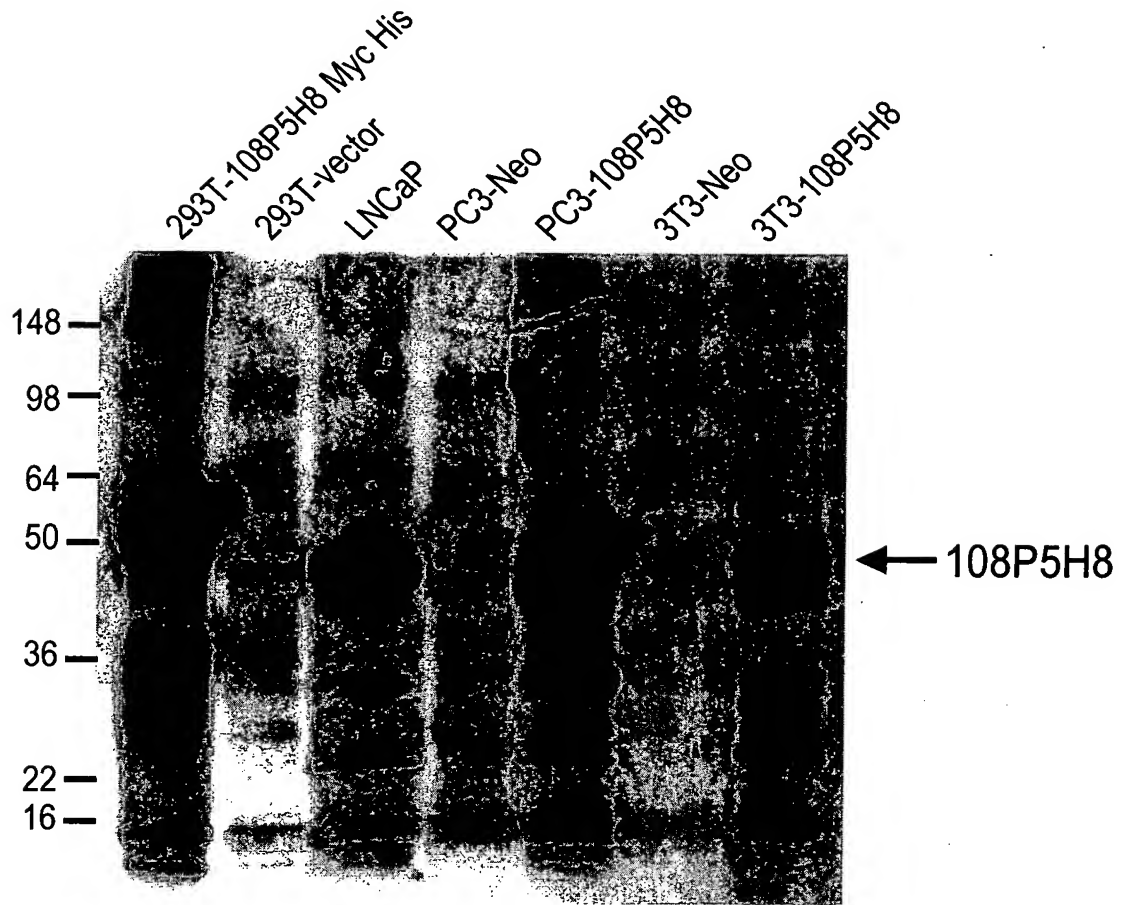


Figure 25: Alignment of 108P5H8 v.1 protein with members of the zinc transporter family.

A-Alignment of 108P5H8 (SEQ. ID. No.: 2576) with the human zinc transporter 4, i.e. gi 11432533 (SEQ. ID. No.: 2577).

Identities = 429/429 (100%), Positives = 429/429 (100%)

```

108P5: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
          MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61   PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120
          PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL
Sbjct: 61   PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120

108P5: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
          YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLNQS 240
          VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLNQS
Sbjct: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLNQS 240

108P5: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
          HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE
Sbjct: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301  YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVVDYIKEALMKIEDVYSVEDL 360
          YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVVDYIKEALMKIEDVYSVEDL
Sbjct: 301  YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVVDYIKEALMKIEDVYSVEDL 360

108P5: 361  NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420
          NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR
Sbjct: 361  NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420

108P5: 421  CANCQSSSP 429
          CANCQSSSP
Sbjct: 421  CANCQSSSP 429

```

B-Alignment of 108P5H8 (SEQ. ID. No.: 2578) with the human zinc transporter ZNT4, i.e. gi 8134840 (SEQ. ID. No.: 2579).

Identities = 428/429 (99%), Positives = 429/429 (99%)

```

108P5: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
          MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61   PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120
          PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL
Sbjct: 61   PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120

108P5: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
          YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLNQS 240
          VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLNQS
Sbjct: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLNQS 240

108P5: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
          HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE

```

Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL

Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR

Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429
CANCQSSSP

Sbjct: 421 CANCQSSSP 429

C-Alignment of 108P5H8 (SEQ. ID. No.: 2580) with the rat zinc transporter ZNT-4, i.e. gi 8134837 (SEQ. ID. No.: 2581).

Identities = 387/430 (90%), Positives = 407/430 (94%), Gaps = 3/430 (0%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
MAG GAWKRLKS+LRKDDAPLFLNDTSADF DE DEGLSRFNKLRVVVADD SEAPER

Sbjct: 1 MAGPGAWKRLKSLLRKDDAPLFLNDTSADFDEGLSRFNKLRVVVADDDSEAPER 60

108P5: 61 PVNGAHTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120
PVNGAHP LQADDDSLDQ+LPLTNSQLSLK+D CDNCSK+RE+LKQKVK RLTIAAVL

Sbjct: 61 PVNGAHPALQADDDSLDQELPLTNSQLSLKMDPCDNCSKRRELLKQKVKTRLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
YLLFMIGELVGGY+ANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPT+RFTFGFHRLE

Sbjct: 121 YLLFMIGELVGGYMANSLAIMTDALHMLTDL SAI ILTLLALWLSSKSPTRRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQ-- 238
VLSAMISV+LVY+LMGFLLYE+QRTIHMNYEINGD+MLITAAGVAVNVIMGFLLNQ

Sbjct: 181 VLSAMISVMLVYVLMGFLLYEAMQRTIHMNYEINGDVMLITAAGVAVNVIMGFLLNQSG 240

108P5: 239 SGHRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 298
H H+HSHSLPSNSP+ S +HGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK

Sbjct: 241 HHHSHSHSHSLPSNSPSMVSS-GHSHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 299

108P5: 299 PEYKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVE 358
PEYKIADPICTY+FSLLVAFTT RIIWDTVVIIIEGVPSHLNVDYIKE+LMKIEDVYSVE

Sbjct: 300 PEYKIADPICTYIFSLVAFTTLRIIWDTVVIIIEGVPSHLNVDYIKESLMKIEDVYSVE 359

108P5: 359 DLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEV 418
DLNIWSLTSGK+TAIVH+QLIPGSSSKWEEVQSKA HLLNTFGMY+CT+QLQSYRQE

Sbjct: 360 DLNIWSLTSGKATAIVHMLIPGSSSKWEEVQSKAKHLLNTFGMYKCTVQLQSYRQEAT 419

108P5: 419 RTCANCQSSS 428
RTCANCQSSS

Sbjct: 420 RTCANCQSSS 429

Figure 26

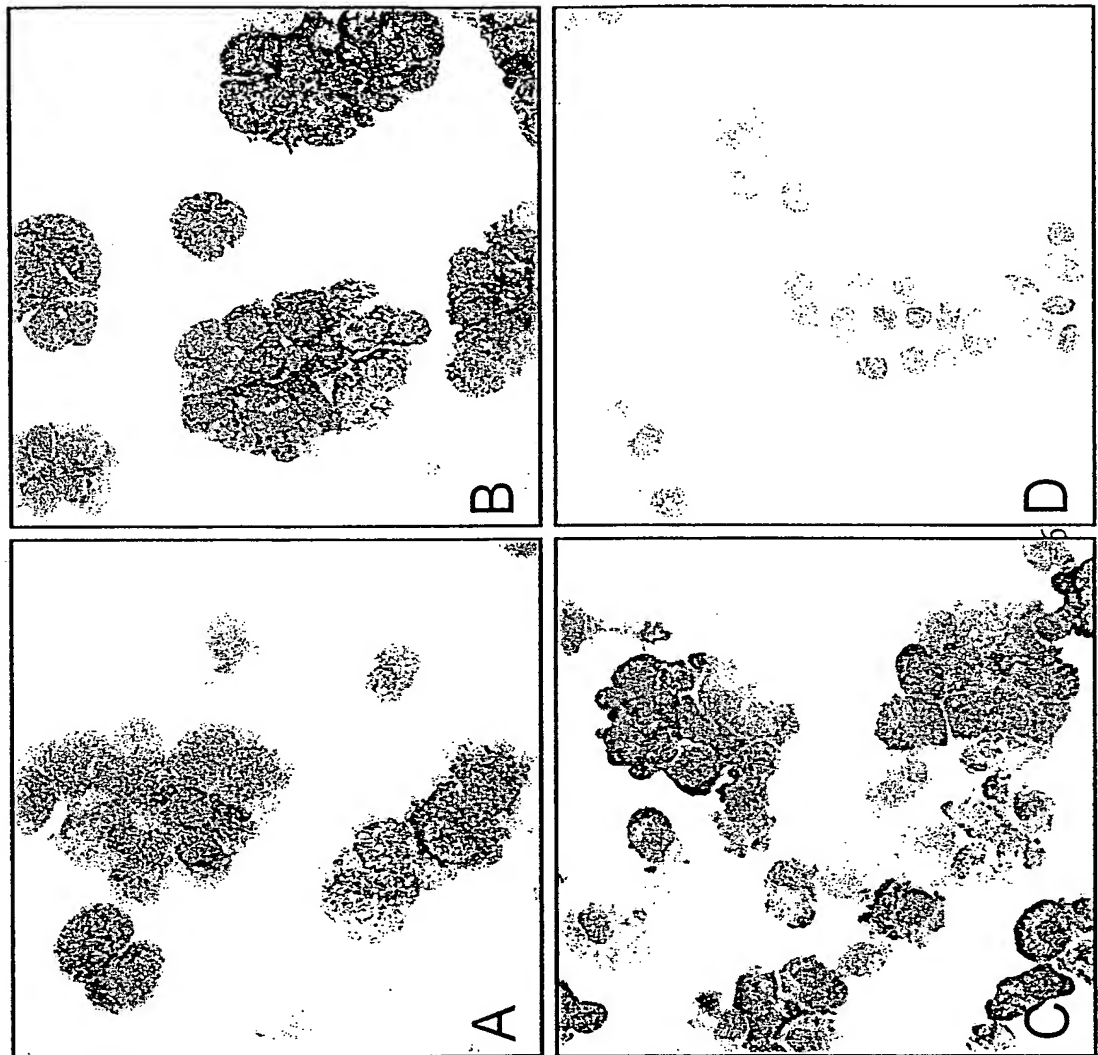


Figure 27

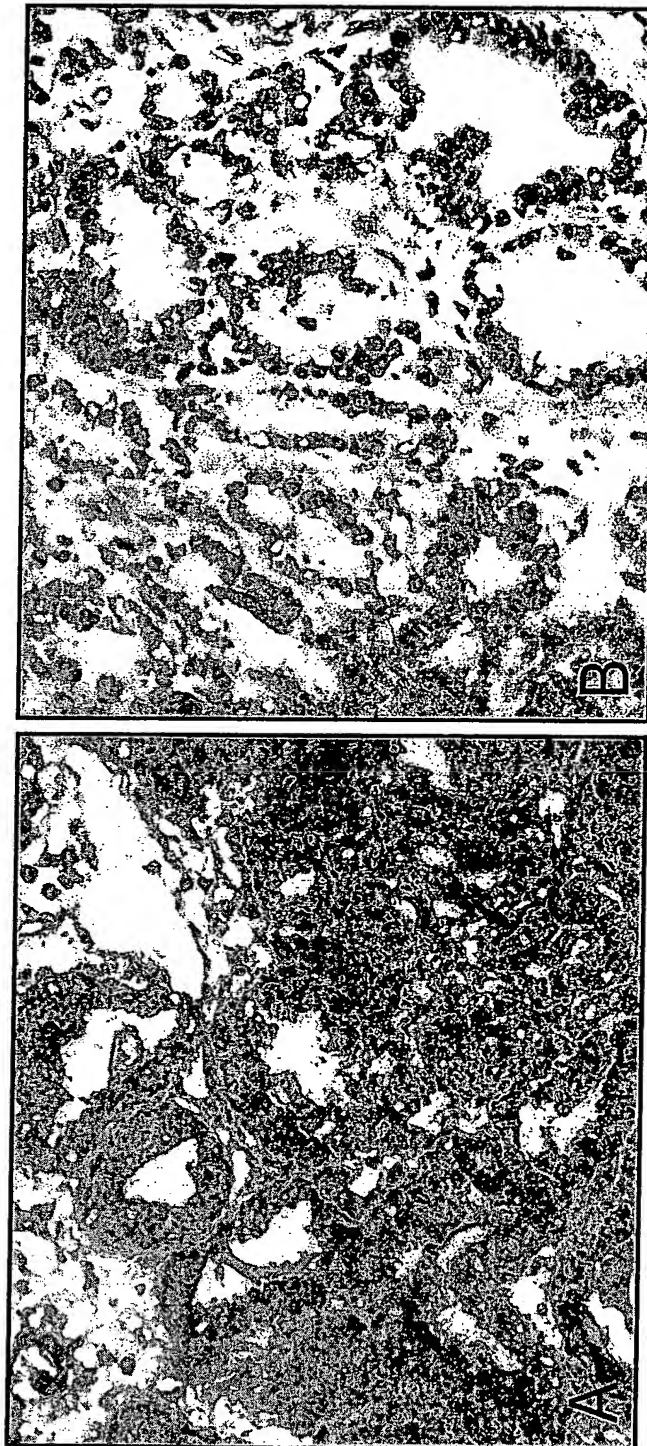
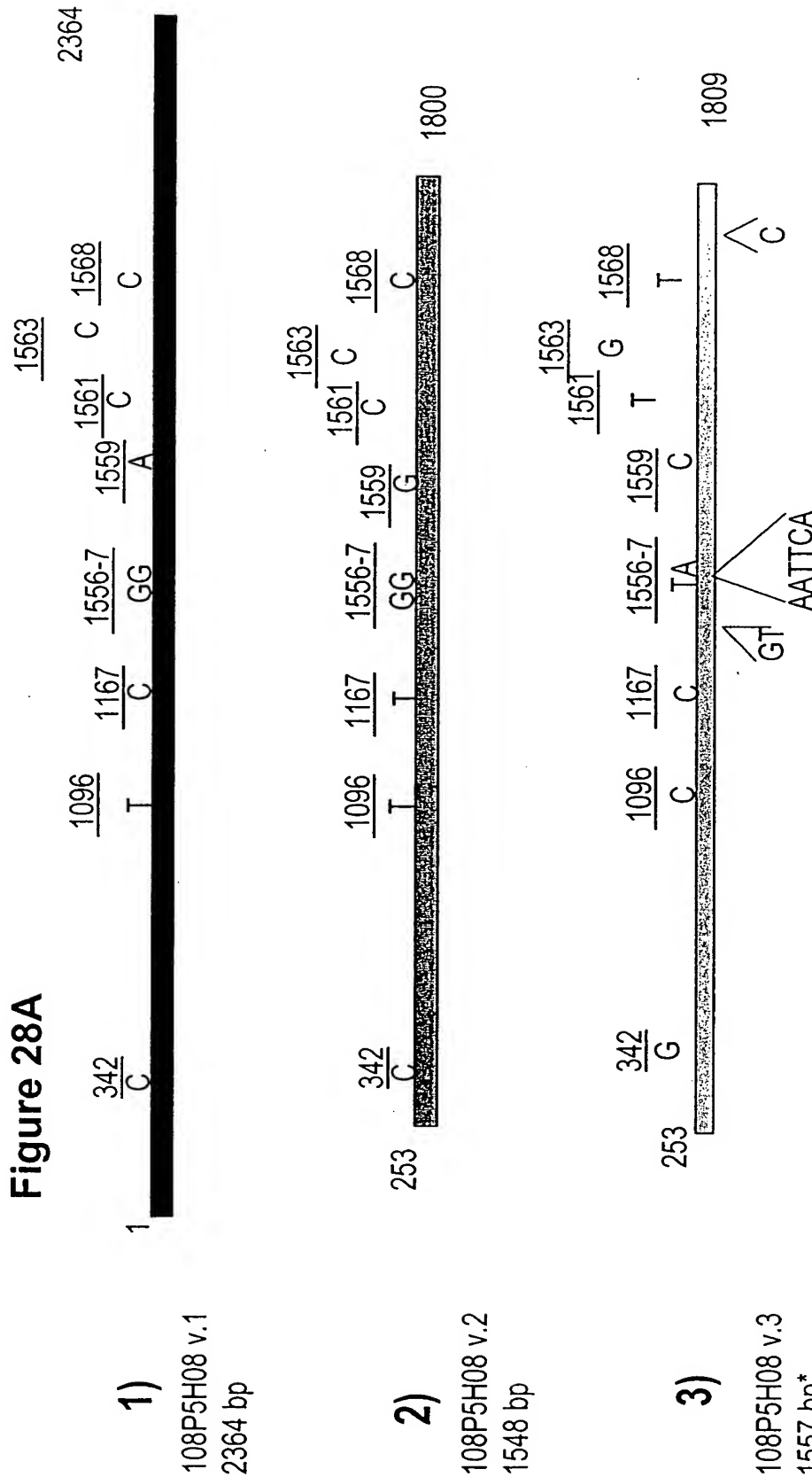


Figure 28A



*There are three insertions in variant 3: GT, AATTCA and C at 1553, 1566 and 1784, respectively; numbering is relevant to variant 1.

Figure 28B

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